DECLARATION

I, Ai FUJII, of HIRAKI & ASSOCIATES, do solemnly and sincerely declare as follows:

1. That I am well acquainted with the English and Japanese languages and am competent to translate from Japanese into English.

2. That I have executed, with the best of my ability, a true and correct translation into English of Japanese Patent Application No. 040523/2001 filed on February 16, 2001, a copy of which I attach herewith.

This 6th day of December, 2005

Ai FUJII

[Name of Document] DESCRIPTION

[Title of the Invention] Full-length Genomic RNA of Papaya Leaf-Distortion Mosaic Virus

[Scope of the Claim]

[Claim 1] An RNA comprising a nucleotide sequence as shown in SEQ ID NO: 1 or a nucleotide sequence complementary to said nucleotide sequence.

[Claim 2] A DNA comprising a nucleotide sequence as shown in SEQ ID NO: 1 in which uracil is replaced by thymine, or a nucleotide sequence complementary to said nucleotide sequence.

[Claim 3] A method for diagnosing infection with papaya leaf-distortion mosaic virus in a plant, comprising determining whether the plant is infected with the virus by detecting an RNA fragment specific in the virus from the plant, wherein the RNA fragment corresponds to a part of a nucleotide sequence as shown in SEQ ID NO: 1.

[Claim 4] A method for diagnosing infection with papaya leaf-distortion mosaic virus, wherein an RNA fragment corresponds to a part of the sequence of the nucleotides 135 - 1574 as shown in SEQ ID NO: 1.

[Claim 5] A method for producing a papaya leaf-distortion mosaic virus-resistant plant, comprising integrating a DNA fragment having a function to impart resistance against papaya leaf-distortion mosaic virus into a plant, wherein the DNA fragment corresponds to a part of a nucleotide sequence as shown in SEQ ID NO: 1.

[Claim 6] A method for producing a foreign protein in a plant comprising the steps of:

1) synthesizing cDNA from genomic RNA of papaya leaf-distortion mosaic virus;

2) adding a nucleotide sequence encoding an amino acid sequence, which can be cleaved with a protease derived from papaya leaf-distortion mosaic virus, to the 5' terminus and the 3' terminus of a gene encoding said foreign protein to obtain a DNA fragment having the nucleotide sequence and a nucleotide sequence of the gene;

3) inserting the DNA fragment of 2) into the cDNA of 1);

4) preparing an RNA by allowing an RNA polymerase to act on the cDNA of 3); and

5) infecting a plant with the RNA of 4).

[Claim 7] A protein selected from the group consisting of the following

(a) to (c):

(a) a protein comprising an amino acid sequence as shown in SEQ ID NO: 4;

(b) a protein comprising an amino acid sequence as shown in SEQ ID NO: 4 having deletion, substitution, or addition of one or more amino acids and having a protease activity to cleave peptide bonds between Gln-Ala, Gln-Ser, and Glu-Gly; and

(c) a protein derived from papaya leaf-distortion mosaic virus encoded by a DNA which hybridizes to a DNA comprising a nucleotide sequence as shown in SEQ ID NO: 3 or a DNA complementary to said nucleotide sequence under stringent conditions, and having a protease activity to cleave peptide bonds between Gln-Ala, Gln-Ser, and Glu-Gly.

[Claim 8] A DNA encoding the protein of claim 7.

[Detailed Description of the Invention]

[Technical Field to Which the Invention Pertains]

The present invention relates to the full-length genomic RNA of papaya leaf-distortion mosaic virus.

[Prior Art]

A problem of a disease called papaya leaf-distortion mosaic disease has arisen in papaya plants in Subtropic areas, causing mosaic symptoms on leaves and ring spots on fruits. It has been shown that this disease is caused by infection with a papaya leaf-distortion mosaic virus (hereinafter referred to as "PLDMV"). PLDMV belonging to the genus Potyvirus of the family Potyviridae is in a string-like shape, and is approximately 800 nanometers in length. The virus is transmitted nonpersistently by aphids. Viral components include its genome consisting of RNA and periplastic proteins surrounding the RNA. The RNA genes contain nucleotide sequences encoding 10 types of proteins required for infection and replication: P1, HC-Pro, P3, 6K1, CI, 6K2, NIa-VPg, NIa-Pro, NIb and CP.

Of these 10 types of proteins encoded by PLDMV genes, only the CP region encoding a periplastic protein has been analyzed so far. No other regions have been analyzed and none of the nucleotide sequences of these regions have been reported.

[Problems to Be Solved by the Invention]

The use of the nucleotide sequence of the full-length genomic RNA

in addition to the CP region would be very useful in elucidating the functions and roles of PLDMV. Accordingly, the object of the present invention is to determine the nucleotide sequence of the full-length genomic RNA of PLDMV.

[Means to Solve the Problems]

To solve the problems, we have determined the full-length nucleotide sequence by cDNA cloning for the entire gene region of PLDMV. Then, we have completed the invention by elucidating the gene structure of regions encoding various proteins from the nucleotide sequence.

Accordingly, the first invention relates to an RNA and a DNA, each of which comprises a nucleotide sequence as shown in SEQ ID NO: 1(or a nucleotide sequence complementary to said nucleotide sequence), or a nucleotide sequence as shown in SEQ ID NO: 1 in which uracil is replaced by thymine(or a nucleotide sequence complementary to said nucleotide sequence), respectively.

The second invention relates to a method for diagnosing infection with PLDMV in a plant, comprising determining whether the plant is infected with the virus by detecting an RNA fragment specific in the virus from the plant, wherein the RNA fragment corresponds to a part of a nucleotide sequence as shown in SEQ ID NO: 1.

The third invention relates to a method for producing a PLDMV-resistant plant, comprising integrating a DNA fragment having a function to impart resistance against PLDMV into the plant, wherein the DNA fragment corresponds to a part of a nucleotide sequence as shown in SEQ ID NO: 1.

The fourth invention relates to a method for producing a foreign protein in a plant comprising the steps of:

1) synthesizing cDNA from genomic RNA of PLDMV;

2) adding a nucleotide sequence encoding an amino acid sequence, which can be cleaved with protease derived from PLDMV, to the 5' terminus and the 3' terminus of a gene encoding said foreign protein to obtain a DNA fragment having the nucleotide sequence and a nucleotide sequence of the gene;

3) inserting the DNA fragment of 2) into the cDNA of 1);

4) preparing an RNA by allowing an RNA polymerase to act on the cDNA of 3); and

5) infecting a plant with the RNA of 4).

The fifth invention relates to a protein selected from the group consisting of the following (a) to (c), and DNAs encoding them:

(a) a protein comprising an amino acid sequence as shown in SEQ ID NO: 4;

(b) a protein comprising an amino acid sequence as shown in SEQ ID NO: 4 having deletion, substitution, or addition of one or more amino acids, and having a protease activity to cleave peptide bonds between Gln-Ala, Gln-Ser, and Glu-Gly; and

(c) a protein derived from PLDMV encoded by a DNA which hybridizes to a DNA comprising a nucleotide sequence as shown in SEQ ID NO: 3 or a DNA complementary to said nucleotide sequence under stringent conditions, and having a protease activity to cleave peptide bonds between Gln-Ala, Gln-Ser, and Glu-Gly.

[Mode for Carrying Out the Invention]

Hereinafter, the present invention will be described in detail.

(1) RNA and DNA

RNA and DNA of the present invention relate to the full-length genomic RNA of papaya leaf-distortion mosaic virus("PLDMV"), and each of them comprises a nucleotide sequence as shown in SEQ ID NO: 1 (or a nucleotide sequence complementary to said nucleotide sequences), or a nucleotide sequence as shown in SEQ ID NO: 1 in which uracil is replaced by thymine(or a nucleotide sequence complementary to said nucleotide sequences), respectively.

DNA of the invention can be obtained from a cDNA library that is synthesized from the viral RNA, or directly from the viral RNA by the RT-PCR method, using appropriate primers which is prepared based on the genetic information shown in SEQ ID NO: 1.

Alternatively, if the information is not used, the DNA of the invention can be obtained, for example, by the following method we have carried out, with modification as needed.

Firstly, viral particles are isolated and purified from leaves of PLDMV-infected Cucumis metuliferus, and then an RNA is extracted from the particles. Using the RNA as a template, cDNA is synthesized with oligo dT primers. The resulting cDNA is incorporated into a phagemide vector

pT7Blue for transformation of E.coli, and thereby obtaining a cDNA library. Then, PCR is performed using the transformed E.coli as a template so as to examine the presence or absence of inserts, and select plasmids containing the cDNA which contains PLDMV gene. Next, the cDNA obtained as described above are cloned. Using the cloned plasmids, nucleotide sequences of the cDNA can be determined by the method, such as dideoxy method. Of the obtained nucleotide sequences, a sequence closest to 5' end of the cDNA is used to prepare a primer. Repetition of the above-mentioned steps can yield a more upstream nucleotide sequence.

RNA of the present invention can be obtained by transcribing the DNA of this invention.

The DNA and RNA of the invention can be used for the diagnosis of infection with PLDMV, production of a PLDMV-resistant plant, and production of a foreign protein in a plant, as described below.

(2) Diagnosing infection with PLDMV in a plant

A method of the invention for diagnosing infection with PLDMV is a method which comprises determing whether the plant is infected with the virus by detecting an RNA fragment specific in the virus from the plant, wherein the RNA fragment corresponds to a part of a nucleotide sequence as shown in SEQ ID NO: 1.

"an RNA fragment corresponds to a part of the nucleotide sequence as shown in SEQ ID NO: 1" as used herein means:

① the RNA fragment comprises a nucleotide sequence which is identical to a part of a nucleotide sequence as shown in SEQ ID NO: 1;

② the RNA fragment comprises a nucleotide sequence which is complementary to a part of a nucleotide sequence as shown in SEQ ID NO: 1;

③ the RNA fragment is that of ① or ②, having deletion, substitution, or addition of one or more nucleotides, and having species-specificity sufficient to use it as an index in diagnosing infection with PLDMV.

An RNA fragment to be detected may correspond to any region of a nucleotide sequence as shown in SEQ ID NO: 1, the RNA fragment corresponding to P1 protein-coding region with high species-specificity is preferred. The P1 protein-coding region corresponds to a part of the sequence of the nucleotides 135 - 1574 as shown in SEQ ID NO: 1.

A method for detecting an RNA fragment includes, but is not limited

to, hybridization method using a labeled DNA or RNA as a probe, and RT-PCR method.

(3) A method for producing a PLDMV-resistant plant

A method for producing a PLDMV-resistant plant of the invention comprises integrating a DNA fragment having a function to impart resistance against PLDMV into a plant, wherein the DNA fragment corresponds to a part of a nucleotide sequence as shown in SEQ ID NO: 1.

"DNA fragment corresponds to a part of a nucleotide sequence as shown in SEQ ID NO: 1" as used herein means:

① the DNA fragment comprises a nucleotide sequence which is identical to a part of a nucleotide sequence as shown in SEQ ID NO: 1 in which uracil is replaced by thymine;

② the DNA fragment comprises a nucleotide sequence which is complementary to a part of a nucleotide sequence as shown in SEQ ID NO: 1 in which uracil is replaced by thymine; and

③ the DNA fragment is that of ① or ②, having deletion, substitution, or addition of one or more nucleotides, and having a function to impart resistance against PLDMV to the plant.

Tennant et al. have reported that they have succeeded in imparting virus resistance to a plant by integrating a region encoding a periplastic protein of papaya ringspot virus type P into the plant (Tennant et al., Phytopathology 84: 1359-1366, 1994). Maiti et al. have reported that they were able to impart virus resistance to a plant by integrating a region encoding a HC-Pro protein of tobacco vein mottling virus into the plant (Maiti, I.B., Murphy, J.F., Shaw, J.G., Hunt, A., 1993, Proc. Narl. Acad. Sci. USA. 90: 6110-6114). Further, Audy et al have reported that they were able to impart virus resistance to a plant by integrating a region encoding an NIb protein of potato virus Y into the plant (Audy, P., Palukaitis, P., Slack, S.A., Zaitlin, M., 1994, Molecular Plant-Microbe Inerractions 7: 15-22). Therefore, a preferable DNA fragment to be integrated into a plant corresponds to a part or whole of regions, including a capsid protein (CP) coding region, a HC-Pro coding region, and/or a NIb coding region.

A PLDMV resistant plant can be produced by integrating a DNA fragment corresponding to a part of a nucleotide sequence as shown in SEQ ID NO: 1 into a plant cell with appropriate promoter and terminator sequences, and allowing the plant cell to regenerate to a plant body. A preferable plant cell, to which the DNA fragment is introduced, is derived from a PLDMV-infectious plant, including papaya, cucumber, Cucumis melo var. conomon, and Cucumis metuliferus. Examples of a form of the plant cell include, but are not specifically limited to, cultured cells, protoplasts, callus, slices of a leaf, embryos. Examples of a promoter sequence used herein include a 35S promoter of cauliflower mosaic virus, and an alcohol dehydrogenase 1 gene promoter. Examples of a terminator sequence used herein include a NOS terminator, and an alcohol dehydrogenase 1 gene terminator. Introduction of the DNA into the plant cell can be performed by various methods known to the skilled in the art. Examples of such a method include methods which use Agrobacterium tumefaciens, Agrobacterium rhizogenes and the like, an electroporation method, a polyethylene glycol method, and a particle gun method. A method for regenerating a plant cell to a plant body may be determined depending on a type of the plant cell. For example, when a plant is papaya, a method by Fitch et al. (Fitch, M. M. M., Manshardt, R. M., Gonsalves, D., Slightom, J. L., Sanford, J. C., 1992, Biotechnology 10: 1466-1472) can be used to regenerate the plant cell to a plant body.

(4) Production of a foreign protein in a plant

A method of the invention for producing a foreign protein in a plant comprises the following steps of 1) to 5).

1) cDNA is synthesized from genomic RNA of PLDMV. An example of the genomic RNA of PLDMV is an RNA comprising a nucleotide sequence as shown in SEQ ID NO: 1. Alternatively, an RNA comprising a nucleotide sequence as shown in SEQ ID NO: 1, having deletion, substitution, or addition of one or more nucleotides, and having infectious ability as a virus, may be used. cDNA can be synthesized by reverse transcription using a genomic RNA as a template. Here, the full-length genomic RNA or a part of the genomic RNA may be used as a template.

2) A nucleotide sequence encoding an amino acid sequence which can be cleaved with a protease derived from PLDMV is added to the 5' terminus

and the 3' terminus of a gene encoding a foreign protein to be produced. Thus, the resulting DNA fragment includes both the nucleotide sequence and the gene. The gene encoding the foreign protein is not specifically limited and may be any gene. Examples of the amino acid sequence which can be cleaved with a protease derived from PLDMV include Gln-Ala, Gln-Ser, Glu-Gly, and the like. These amino acid sequences can be cleaved with NIa-Protease (hereinafter referred to as "NIa-Pro") derived from PLDMV.

3) The DNA fragment of 2) is inserted into the cDNA of 1). The DNA fragment of 2) may be inserted into any position between P3 region and CP region of the cDNA of 1). The gene encoding the foreign protein can be inserted with, e.g., restriction enzymes.

4) RNA polymerase is allowed to act on the resulting cDNA of 3), and thereby synthesizing an RNA.

5) The RNA of 4) is allowed to infect a plant.

(5) A protein having a protease activity

The proteins of this invention are selected from the group consisting of the following (a) to (c):

(a) a protein comprising an amino acid sequence as shown in SEQ ID NO: 4;

(b) a protein comprising an amino acid sequence as shown in SEQ ID NO: 4 having deletion, substitution, or addition of one or more amino acids, and having a protease activity to cleave peptide bonds between Gln-Ala, Gln-Ser, and Glu-Gly; and

(c) a protein derived from PLDMV encoded by a DNA which hybridizes to a DNA comprising a nucleotide sequence as shown in SEQ ID NO: 3 or a DNA complementary to said nucleotide sequence under stringent conditions, and having a protease activity to cleave peptide bonds between Gln-Ala, Gln-Ser, and Glu-Gly.

The protein of (a) is NIa-Pro (a fragment having a protease activity of NIa) which was obtained from PLDMV used in the following Example.

The protein of (b) is a protein in which mutation is introduced without decreasing or losing a protease activity of the original protein. Examples of such mutation include, but are not limited to, naturally-occurring and artificial mutations. An example of a technique to cause an artificial mutation is, but is not limited to, site-specific

mutagenesis (see, Nucleic Acids Res. 10, 6487-6500, 1982). The number of amino acids mutated is not limited, provided that it does not lose a protease activity of the protein to cleave peptide bonds between Gln-Ala, Gln-Ser and Glu-Gly. Generally, the number is within 30 amino acids, preferably within 20 amino acids, more preferably within 10 amino acids, and most preferably within 5 amino acids.

The protein of (c) is a protease derived from PLDMV which can be obtained by using a hybridization of DNAs. "Stringent conditions" used for the protein of (c) means conditions under which only specific hybridization occurs and non-specific hybridization does not occur. Such conditions are generally "1xSSC, 0.1%SDS, 37℃", preferably "0.5xSSC, 0.1%SDS, 42℃", more preferably "0.2xSSC, 0.1%SDS, 65℃". A DNA obtained by such hybridization generally shows high homology with a DNA comprising a nucleotide sequence as shown in SEQ ID NO: 3. The term "high homology" used herein means 60% or more of homology, preferably 75% or more of homology, and more preferably 90% or more of homology.

The proteins of the invention (proteins of (a) to (c)) have a protease activity to cleave peptide bonds between Gln-Ala (between Q-A), Gln-Ser (between Q-S), and Glu-Gly (between E-G). This can be presumed from the following.

The polyproteins of Potyvirus include 10 types of proteins, such as P1, HC-Pro, P3, 6K1, CI, 6K2, NIa-VPg, NIa-Pro, NIb, and CP. Of these proteins, P1 and HC-Pro has self-cleavage activity, P3 and the other proteins can be cleaved with NIa-Pro. That is, NIa-Pro has a function to recognize and cleave peptide bonds between P3-6K1, 6K1-CI, CI-6K2, 6K2 - NIa-VPg, NIa-VPg - NIa-Pro, NIa-Pro - NIb, and NIb-CP. Table 1 shows amino acid sequences at the N terminus and at the C terminus of each protein composing the polyprotein of Potyvirus. As shown in the table, for PLDMV, there are three types of comnbinations of N-terminus amino acid of one protein and C-terminus amino acid of another protein: Gln and Ala (Q and A), Gln and Ser (Q and S), as well as Glu and Gly (E and G). Therefore, NIa-Pro from PLDMV is thought to cleave the peptide bonds between Gln-Ala, Gln-Ser, and Glu-Gly.

Table 1 also shows amino acid sequences at the N terminus and the C terminus of each protein composing the polyprotein of Potyviruses other than PLDMV. The cleavage sites of NIa-Pro derived from each virus

other than PLDMV, which are presumed from datas in this table, are thought to be quite different from those of NIa-Pro derived from PLDMV.

Table 1

Literature in which sequences are described and Accession numbers of Gen Bank

Virus	P1	/Hcpro	/P3	/6K1	/CI	/6K2	/NIa-Vpg/NIa-pro/NIb	/CP
PLDMV *1	M	Y/S	G/G	Q/A	Q/S	Q/S	E/G E/G	Q/S Q/S Y
PVY *1	M	F/S	G/G	Q/R	Q/S	Q/A	Q/G E/A	Q/A Q/A M
PepMoV *1	M	Y/S	G/G	Q/R	Q/S	Q/S	Q/G E/A	Q/A Q/S M
TVMV *1	M	F/S	G/G	Q/A	Q/S	Q/S	Q/G E/S	Q/G Q/S V
TEV *1	M	Y/S	G/G	Q/A	Q/S	Q/S	Q/G E/G	Q/G Q/S Q
SbMV *1	M	Y/S	G/G	Q/A	Q/S	Q/S	Q/G E/S	Q/G Q/S Q
PRSV *1	M	Y/N	G/G	Q/A	Q/S	Q/S	Q/G E/G	Q/S Q/S N
PSbMV *1	M	F/S	G/G	Q/A	Q/S	Q/S	E/G E/A	Q/S Q/A M
TuMV *1	M	F/S	G/G	Q/A	Q/T	Q/S	E/A E/S	Q/T Q/A L
JGMV *1	M	Y/S	G/G	E/R	E/G	E/N	E/G E/G	E/S Q/S I
PPV *1	M	Y/S	G/G	Q/S	Q/S	Q/T	Q/G E/S	Q/S Q/A V
JYMV-JI *2	M	Y/S	G/G	Q/A	Q/A	Q/S	E/A E/S	Q/M Q/S V
JYMV-M *3	M	F/A	G/G	Q/A	Q/G	Q/S	E/A E/S	Q/M Q/S V
SPFMV *4	M	Y/S	G/G	Q/G	Q/S	Q/T	Q/G E/S	Q/T Q/S V
RMV *5	M	Y/S	G/G	Q/A	Q/S	Q/S	E/G E/S	Q/S E/A L
PSV *6	M	Y/S	G/G	Q/A	Q/S	Q/G	Q/G E/S	Q/S Q/S Q
PVA *7	M	L/S	S/A	Q/A	Q/A	Q/S	Q/S E/S	Q/G Q/A V

*1:Shukla, D.D., Ward, C.W. and Brunt, A.A. (1994). The potyviridae. CAB international, West Sussex., *2:AB016500, *3:AB027007, *4:NC 001841, *5:NC 001814, *6:NC 001723, *7:NC 001649

[Examples]

Hereinafter, the present invention will be described more specifically by use of the following examples.

[Example 1] Determination of the nucleotide sequence of PLDMV periplastic protein gene

(1) Isolation and purification of a virus

450 ml of 0.5M citrate buffer containing 0.56g of sodium sulfite (this buffer had been prepared with 0.5 M citric acid to pH 7.0) was added to 140 g of Cucumis metuliferus inoculated with PLDMV, and then ground with a blender. The homogenate was squeezed through cotton cloth. Then, carbon tetrachloride was added to the filtrate, allowing the carbon tetrachloride to be 6% of the whole filtrate. After vigorous mixing, the filtrate was centrifuged at 6,000g and 4℃ for 15 min, so that the supernatant was obtained. To 500 ml of the supernatant, 37.6g of polyethylene glycol 6000, 2.92g of sodium chloride, 10ml of Triton x100 were added. The mixture was stirred at 4℃ for 90 min, and then centrifuged

at 6,000g and 4℃ for 15 min. To the pellet precipitated after centrifugation, 0.1M citrate buffer containing 0.01M sodium sulfite (this buffer had been prepared with 0.1M citric acid to pH 7.0 and hereinafter referred to as a CD buffer) was added for re-suspension. The mixture was centrifuged at 6,000g and 4℃ for 15 min, thereby obtaining the supernatant. Next, 30ml of the supernatant was superposed over a 40% sucrose solution (prepared with CD buffer), and then centrifuged at 125,000g for 90 min. Then the pellet was resuspended with 20ml of a CD buffer, followed by centrifugation at 6,000g and 4℃ for 15 min, thereby obtaining the supernatant. Subsequently, 10ml of the supernatant was layered on 2ml of a 40% sucrose solution (prepared with a CD buffer), followed by centrifugation at 125,000g for 90 min. The pellet was resuspended with 2.5ml of a CD buffer, centrifuged at 6,000g and 4℃ for 15 min, thereby obtaining the supernatant. Then, the supernatant was layered on a linear density gradient of a cesium sulfate centrifugation (10-41%, Hitachi RPS40T rotor was used at 38,000rpm and 6℃ for 15 hours). Thus the obtained white band of a virus fraction was collected, diluted with a CD buffer, and then centrifuged at 238,000g and 4℃ for 90min. The precipitated virus pellet was resuspended with 0.3ml of 0.01M citrate buffer (pH 7.0), thereby obtaining a purified sample of the virus.

(2) Preparation of PLDMV-RNA

RNA was extracted from the purified PLDMV above using a commercially available nucleic acid extraction kit, Sepagene (Sanko Junyaku Co., Ltd.). Extraction was performed according to the attached instructions.

(3) Construction and screening of a cDNA library

Since the viral RNA belonging to the genus Potyvirus has a poly A sequence at its 3'terminus, a double-stranded cDNA was synthesized using an oligo dT primer. A series of steps was taken with a commercially available cDNA synthesis kit (CLONTECH)according to the instructions attached to the kit. Adapter primers were linked to both ends of the synthesized cDNA. Next, PCR was performed using a downstream primer (NIb1) which is complementary to a known sequence of the NIb protein region of PLDMV, and using an upstream primer (AP1) of a sequence contained in the adapter primer. The amplified product was subjected to column

purification, and then inserted to a cloning site of a phagemide vector pT7Blue (Novagen). Column purification was performed using SizeSep400 Spum Columns (Amersham Pharmacia Biotech) according to the attached instructions. The reaction product was transferred into E.coli strain JM109.

A small amount of plasmids were rapidly prepared from the PLDMV cDNA library obtained as described above, thereby obtaining a clone (NIb-99) having an approximately 2Kb insert. The nucleotide sequence of the cDNA library was determined by the dideoxy method and analyzed with DNASIS (Hitachi Soft Engineering, Ver. 7.0).

Based on the upstream sequences of the determined nucleotide sequence, complementary primers were constructed. By repetition of the above described PCR, cloning, and sequencing, each clone (NIa-41, CI-64, 6K1-46, HC-23, and P1-40) was obtained from downstream to upstream. Further, PCR was performed using primers complementary to sequences upstream of CI-64, primers homologous to sequences upstream of HC-23, and using cDNA library as a template. Thus, a clone (P16K1-11) having an approximately 4kb insert was obtained. The upstream sequence of PLDMV genome was determined from these clones.

(4) Determination of the 5' terminal sequence

Cloning of the 5' terminal portion of PLDMV gene has been tried several times by the 5' RACE method as described above. However, no plasmid containing this sequence was obtained. Then, primer extension was performed using the clone (P1-40) obtained in (3) above as a template, suggesting that 14 bases from the 5' terminus of PLDMV were not decoded yet. To elucidate the above sequence, improvement in the RNA purification method and the cloning method were tried.

TE (10mM Tris-HCl pH 8.0, 1mM EDTA) 68 μl, 10 μl of 20xSSC (3M NaCl, 0.3M sodium citrate pH 7.0), 2μl of 20%SDS, and 20 μl of proteinase K (10mg/ml) were added to 100 μl of the purified PLDMV, and the mixture was kept at 37℃ for 60 min. Next, 100 μl of 0.5% bentonite solution, and 200 μl of TE saturated phenol solution were added to the mixture. Then the mixture was shaken and centrifuged with an eppendolf small type centrifuge for 3 min, thereby obtaining the aqueous layer. After repeating the phenol extraction process as described above, 200 μl

chloroform was added to the aqueous layer. The mixture was shaken, centrifuged with an eppendolf small type centrifuge for 3 min, thereby obtaining the aqueous layer. To the thus obtained aqueous layer, 25 μl of 3M sodium acetate solution (pH 5.2), and 500 μl of ethanol were added. The mixture was kept at -80℃ for 30 min, centrifuged with an eppendolf small type centrifuge for 10 min, thereby obtaining RNA as a precipitate. Next, 1 ml of 80% ethanol was added to the precipitate, followed by centrifugation with an eppendolf small type centrifuge for 3 min. Then, ethanol was removed, and RNA was dissolved in 100 μl of TE. In order to further increase purity of the RNA extract, the following steps were taken. 100 μl of 4M lithium chloride was added to the RNA solution, and then kept on ice for 4 hours, followed by centrifugation with an eppendolf small centrifuge for 10 min. 400 μl of 80% ethanol was added to the RNA precipitate, centrifuged for 3 min with an eppendolf small type centrifuge. After ethanol was removed, the RNA was dissolved in 12.5 μl of distilled water. Subsequently, 10 μl of 3M sodium acetate solution (pH 5.2) and 250 μl of ethanol were added to the mixture, kept at -80℃ for 30 min, and then centrifuged for 10 min with an eppendolf small type centrifuge, thereby obtaining RNA as the precipitate. One ml of 80% ethanol was added to the RNA, centrifuged for 3 min with an eppendolf small type centrifuge. After removal of ethanol, the RNA was dissolved in 10 μl of distilled water.

The cloning method was improved as follows. 1 μl of the complementary primer (P1-4)100pM solution that had been prepared based on the sequence of the upstream portion of the clone (HC-23), 2 μl of the purified PLDMV-RNA above, and 7 μl of distilled water were mixed and kept at 65℃ for 5 min. Next, 9.2 μl of distilled water, 9.0 μl of 4xRT buffer (CLONTECH), 1.6 μl of 40U/μl RNase Inhibitor (CLONTECH), 3.7 μl of dNTPmix (10mM each), 0.5 μl of AMV Reverse Transcriptase (CLONTECH) were added to the solution, and then kept at 42℃ for 30 min. Thus ssDNA was synthesized. To this solution, 1 μl of 0.5M EDTA (pH 8.0) was added and mixed, and then placed on ice. Subsequently, 2 μl of 6N NaOH was added to the mixture, and kept at 65℃ for 30 min. After RNA was degraded, 2 μl of 6N acetic acid was added to and mixed with the mixture, followed by addition of 16 μl of distilled water. DNA was purified from the solution using a QIA quick PCR Purification Kit (QIAGEN). Purification

was performed according to the attached instructions.

The above ssDNA 2.5 μl was added with 2 μl of anchor primer (Zhi, 1996), 5 μl of 2xSingle-stranded Ligation Buffer (CLONTECH), 0.5 μl of 20U/μl T4 RNA Ligase (CLONTECH), and 0.5 μl of 50U/μl T4 RNA Ligase (TAKARA), and then allowed to stand at 22℃ overnight. Next, nested PCR was performed using this solution as a template, and a primer set (AP-B, P1-3) containing each sequence of the anchor primer and the complementary primer (P1-4) that had been used for reverse transcription reaction. Furthermore, nested PCR was performed using the reaction product as a template, and the more inward primer set (AP-C, P1-7). Then, cDNA was purified from the reaction product using a QIA quick PCR Purification Kit (QIAGEN), inserted into the cloning site of a phagemide vector pT7Blue (Novagen), thereby transferring into E.coli strain JM109. About 200 clones were selected from the cDNA library by colony PCR, thereby obtaining two clones (P1-7-6, P1-7-103) containing PLDMV 5' terminal sequences. Therefore, the 5' terminal sequence of PLDMV genome was decoded from these clones.

It was found that PLDMV genomic RNA comprised 10,155 bases, and had a poly A sequence at the 5' terminus followed by 135 bases of an untranslated region. There was an ORF starting from the initiation codon AUG at the 136th base from the 5' terminus and ending at the termination codon UAG at the 9943rd base. At the 3' terminus, there was another untranslated region comprising 208 bases following a termination codon, and a poly A sequence existed following A at the 10,155th base, as well.

A polyprotein encoded by ORF consisted of 3269 amino acids. With reference to Shukla et al. 's report (Shukla, D.D., Ward, C.W. and Brunt, A.A., 1994, The potyviridae, CAB international, West Sussex), the positions of various protein genes of PLDMV were specified. Therefore, it was shown that P1 consists of 480 amino acids , HC-Pro of 458 amino acids, P3 of 348 amino acids, 6K1 of 52 amino acids, CI of 635 amino acids, 6K2 of 52 amino acids, NIa-VPg of 187 amino acids, NIa-pro of 243 amino acids, NIb of 521 amino acids, and CP of 293 amino acids, all of which are shown in SEQ ID NOs: 1 and 2.

[Effects of the Invention]

Elucidation of various protein gene structures of PLDMV of this

invention enables detection of PLDMV gene by the RT-PCR method using the primers which are constructed based on the gene sequence. For example, there is a report that BYMV gene was detected from an infected plant by the RT-PCR method using primers that had been constructed based on the nucleotide sequence of bean yellow mosaic virus (BYMV) (Vunsh R, Rosner A, Stein A Ann Appl Biol 117: 561-569, 1990). Particularly, detection of P1 protein region with high species specificity allows highly accurate detection. For example, it has been reported that introduction of the periplastic protein gene of papaya ringspot virus type P (PRSV-P) into a papaya plant resulted in a virus-resistant plant (Tennant et al., Phytopathology 84; 1359-1366, 1994). That is, production of a PLDMV-resistant plant becomes possible by integrating the gene into the plant using genetic recombination techniques. Moreover, it has been reported that a foreign protein was produced in a plant body using an infectious clone of potato X virus or of tobacco mosaic virus as a vector (Ryabov, E.V. et al., Virology 242: 303-313, 1998). That is, insertion of a gene encoding a foreign protein into a PLDMV infectious clone allows use of the clone as an expression vector.

[Sequence Listing]

SEQUENCE LISTING

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Tetsuo Maoka

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cgu uuu gag uug ccg ccu uac uuu aug gcu uca cuu gua uau cau gau 5451
Arg Phe Glu Leu Pro Pro Tyr Phe Met Ala Ser Leu Val Tyr His Asp
1760 1765 1770

ggc agc aug cac ccu gaa auu cac aag cau uua auu ccu uac aag uua 5499
Gly Ser Met His Pro Glu Ile His Lys His Leu Ile Pro Tyr Lys Leu
1775 1780 1785

gau gaa ucu gaa auu caa cuu agu gcc aug gcu uuu aac uuu acc gua 5547
Asp Glu Ser Glu Ile Gln Leu Ser Ala Met Ala Phe Asn Phe Thr Val
1790 1795 1800

aca ucu auu ugg cua gau ugu aaa uuu uau gac agu aua gga auc cau 5595
Thr Ser Ile Trp Leu Asp Cys Lys Phe Tyr Asp Ser Ile Gly Ile His
1805 1810 1815 1820

cuu gau uua ccg cgc gaa gca aaa auu cca uuc cau ugu aga gaa uuc 5643

Leu Asp Leu Pro Arg Glu Ala Lys Ile Pro Phe His Cys Arg Glu Phe
1825 1830 1835

cca gau aug aaa uac cga cac uug ugg gaa gau auu cuc aaa auc aag 5691
Pro Asp Met Lys Tyr Arg His Leu Trp Glu Asp Ile Leu Lys Ile Lys
1840 1845 1850

agc aua aau ugu uuu ggu aga aug agu guu guu agc gca aca aaa gua 5739
Ser Ile Asn Cys Phe Gly Arg Met Ser Val Val Ser Ala Thr Lys Val
1855 1860 1865

gca uau aca cuu aaa aca gac auu cau uca auu gga aaa acu cuc gga 5787
Ala Tyr Thr Leu Lys Thr Asp Ile His Ser Ile Gly Lys Thr Leu Gly
1870 1875 1880

uau auu gac gcc cuc uug caa gaa gaa uau aga aaa cag cau cau uuu 5835
Tyr Ile Asp Ala Leu Leu Gln Glu Glu Tyr Arg Lys Gln His His Phe
1885 1890 1895 1900

aaa gca aug aca agu aac gca ugu agu ggg aac acu uuu uca aug cua 5883
Lys Ala Met Thr Ser Asn Ala Cys Ser Gly Asn Thr Phe Ser Met Leu
1905 1910 1915

agc aua gca aau gca aua cgg aac cac uau gcu aag gac uac acu gcu 5931
Ser Ile Ala Asn Ala Ile Arg Asn His Tyr Ala Lys Asp Tyr Thr Ala
1920 1925 1930

ggc aau auu cag aaa uug cag gca gca aag aau caa aua cug gaa uuc 5979
Gly Asn Ile Gln Lys Leu Gln Ala Ala Lys Asn Gln Ile Leu Glu Phe
1935 1940 1945

guc aau uua aau cuu gau ccu ucg gcg aaa ugc gga uuc caa gag uuc 6027
Val Asn Leu Asn Leu Asp Pro Ser Ala Lys Cys Gly Phe Gln Glu Phe
1950 1955 1960

gga gcu uua gaa cua guu acc cau cag agc agg caa gaa auu uca aaa 6075

Gly Ala Leu Glu Leu Val Thr His Gln Ser Arg Gln Glu Ile Ser Lys
1965 1970 1975 1980

uuu cua aau cug aga ggu aag ugg aau aag uca cua auu aca cgu gau 6123
Phe Leu Asn Leu Arg Gly Lys Trp Asn Lys Ser Leu Ile Thr Arg Asp
1985 1990 1995

auc uua guu uug uua ggu guc acu auu ggu ggu uuc ugg aug aua ugg 6171
Ile Leu Val Leu Leu Gly Val Thr Ile Gly Gly Phe Trp Met Ile Trp
2000 2005 2010

gau aag uuc aaa uca aac auu gaa gaa guu cau cau gaa gga aag agg 6219
Asp Lys Phe Lys Ser Asn Ile Glu Glu Val His His Glu Gly Lys Arg
2015 2020 2025

aag acu caa aag cuu aaa uuu cgg gau gcu cgc gau aag aaa aug ggu 6267
Lys Thr Gln Lys Leu Lys Phe Arg Asp Ala Arg Asp Lys Lys Met Gly
2030 2035 2040

cga gaa gua uau gga gac gac ggu acu auu gaa cau uac uuu gga ucg 6315
Arg Glu Val Tyr Gly Asp Asp Gly Thr Ile Glu His Tyr Phe Gly Ser
2045 2050 2055 2060

gca uac guc aag aga ggu gca guu aag ggc cag aag aga gga aug ggc 6363
Ala Tyr Val Lys Arg Gly Ala Val Lys Gly Gln Lys Arg Gly Met Gly
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gaa aaa uca aga cgu uuc guu agu aug uau gga guu aau uua gaa gau 6411
Glu Lys Ser Arg Arg Phe Val Ser Met Tyr Gly Val Asn Leu Glu Asp
2080 2085 2090

uuu gcu uuu auu aga uac aua gau ccc aua acu gga gca acg cgu gau 6459
Phe Ala Phe Ile Arg Tyr Ile Asp Pro Ile Thr Gly Ala Thr Arg Asp
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Glu Ser Pro Leu Thr Asp Val Glu Leu Val Gln Ala His Phe Gly Glu
2110 2115 2120

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Ile Arg Asp Lys Met Leu Asp Glu Gly Leu Ile Asp Arg Gln His Ile
2125 2130 2135 2140

uua aau aaa cca ggu uug aca gca uac uua guu aag gac ggg guu aag 6603
Leu Asn Lys Pro Gly Leu Thr Ala Tyr Leu Val Lys Asp Gly Val Lys
2145 2150 2155

ucc auc aug aaa gua gau uug caa cca cac aau ccu cua cuc aua ugc 6651
Ser Ile Met Lys Val Asp Leu Gln Pro His Asn Pro Leu Leu Ile Cys
2160 2165 2170

aaa aac aaa gcg aca aua gca ggg uuu ccu gag aag gag uuu guu uug 6699
Lys Asn Lys Ala Thr Ile Ala Gly Phe Pro Glu Lys Glu Phe Val Leu
2175 2180 2185

cga caa acg gac aaa gca uau gaa gua agu aga gag gaa cua cca gaa 6747
Arg Gln Thr Asp Lys Ala Tyr Glu Val Ser Arg Glu Glu Leu Pro Glu
2190 2195 2200

cgg aau gaa gac guu ucu uuu gaa gga gcc uca agu gug aag gga uug 6795
Arg Asn Glu Asp Val Ser Phe Glu Gly Ala Ser Ser Val Lys Gly Leu
2205 2210 2215 2220

cgc gau uac aau ggu gua gcc agc gcu auu ugc caa cuc aca aac aac 6843
Arg Asp Tyr Asn Gly Val Ala Ser Ala Ile Cys Gln Leu Thr Asn Asn
2225 2230 2235

uca aau ggu cgg ucc acc aca acu uau ggg guu ggc uuu ggc uca uac 6891
Ser Asn Gly Arg Ser Thr Thr Thr Tyr Gly Val Gly Phe Gly Ser Tyr
2240 2245 2250

auc aua guu aau agg cac uug uuu aaa gaa aau aau ggg aau uua uug 6939

Ile Ile Val Asn Arg His Leu Phe Lys Glu Asn Asn Gly Asn Leu Leu
2255 2260 2265

auc aaa ucg acg cau gga aau uuc aau auc agg aac ucc aag caa auu 6987
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2285 2290 2295 2300

aaa gac uuc cca ccc uuu gca cag agg uua cga uuu aga aau cca aua 7083
Lys Asp Phe Pro Pro Phe Ala Gln Arg Leu Arg Phe Arg Asn Pro Ile
2305 2310 2315

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Val Gly Glu Ser Ile Cys Leu Val Gly Asn Thr Phe Gln Glu Lys Tyr
2320 2325 2330

aau gca agc auc guu ucu gag aca agc aaa aca uuc cca cga guu gaa 7179
Asn Ala Ser Ile Val Ser Glu Thr Ser Lys Thr Phe Pro Arg Val Glu
2335 2340 2345

ggu agu uuu ugg aaa cau ugg auu aau aca acg gaa gga cau ugu gga 7227
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2350 2355 2360

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2365 2370 2375 2380

uua aug agu cau aag uac gau cau aau uau uuc ucg aac uuu gac gac 7323
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2385 2390 2395

gcg uuu gaa ggc gau uau auu aac aag uug aag gaa cug aaa ugg gag 7371

Ala Phe Glu Gly Asp Tyr Ile Asn Lys Leu Lys Glu Leu Lys Trp Glu
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Gln Asn Trp Thr Tyr Asn Val Asn Thr Val Ser Trp Gly Asn Met Lys
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2465 2470 2475

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2480 2485 2490

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2495 2500 2505

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Val Asp Thr Glu Arg Phe Glu Asp Ala Val Gly Gln Val Ile Glu Ile
2545 2550 2555

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2560 2565 2570

cag auc uuu gaa uca uug aac aug aaa gcg gca guc ggu gcg uug uac 7899
Gln Ile Phe Glu Ser Leu Asn Met Lys Ala Ala Val Gly Ala Leu Tyr
2575 2580 2585

agu ggu aag aaa aag gcg uac uuc gaa aau ucc aca uuu gau gau cga 7947
Ser Gly Lys Lys Lys Ala Tyr Phe Glu Asn Ser Thr Phe Asp Asp Arg
2590 2595 2600

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2625 2630 2635

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2640 2645 2650

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2655 2660 2665

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Asp Leu Asn Met Lys Cys Pro Trp Thr Val Gly Met Thr Lys Phe Tyr
2670 2675 2680

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Cys Gly Trp Asn Asp Leu Leu Gly Lys Leu Pro Asp Gly Trp Ile Tyr
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Trp Asp Arg Ser Val Lys Pro Glu His Arg Leu Glu Ala Ile Cys Ala
2880 2885 2890

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2945 2950 2955

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Val Ser His Gln Ser Ala Leu Asp Ala Gly Lys Pro Thr Ala Glu Asn
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2990 2995 3000

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3070 3075 3080

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3085 3090 3095 3100

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3165 3170 3175 3180

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3185 3190 3195

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Ser Leu Lys Arg Ala Ile Lys Glu Lys Asp Leu Thr Ala Ser Gly Ser
65 70 75 80

Cys Phe His Cys Gly Leu Arg Ala Gln Ile Gly Glu Gly Arg Lys Arg
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Val Glu Leu Ala Pro Ile Ser Val Met Glu Asp Val Glu Thr Val Glu
100 105 110

Gln Val Leu Val Pro Cys Met Val Glu Glu Lys Tyr Tyr Lys Glu Val
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Ser Asn Phe Gln Lys Ala Thr Leu Ile Asp Lys Pro Lys Leu Thr Ile
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Ala Pro Val Leu Met Ala Gln Pro Ala Gln Val Pro Arg Pro Ala Val
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Glu Asn Lys Val Leu Glu Glu Glu Thr Gln Cys Ala Ser Asp Ala Ala
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Leu His His Leu Asp Asp Val His Ala Cys Arg Ala Arg Ala Gln Val
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225 230 235 240

Ser Phe Phe Asn Gln Thr His Arg Glu Asp Arg Tyr Glu Gly Lys Val
245 250 255

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Tyr Thr Phe Lys Lys Gln Arg Asn Asp Lys Lys Arg Val Leu Lys Glu
325 330 335

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Arg Gly Ser Leu Arg Val Gln Cys Thr Lys Asn Cys Gly Ser Arg Val
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385 390 395 400

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His Ile Ile Gln Tyr Asp Lys Phe Arg Gly Leu Ser Gly Arg His Phe
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Ser Asp Ala Gly Leu Ser Phe Trp Lys Gly Phe Asp Arg Gln Phe Ile
485 490 495

Asp Ile Arg Asp Arg Pro Lys Asn Ala His Glu Cys Lys Ala Thr Ile
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Met Leu Ser Gln Glu Glu Glu Leu Glu Ser Phe Arg Arg Lys Arg Ser
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Gln Leu Ala Ser Lys Leu Ser Ser Leu His Ile Lys Phe Pro Tyr Val
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Asp His Phe Leu Asn Arg Tyr Glu Asn Ser Leu Asn Arg Met Asn Thr
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Val Trp Gly Glu Arg Gly Tyr His Ala Lys Arg Phe Phe Leu Asn Phe
690 695 700

Phe Glu Lys Val Asp Ser Thr Asp Gly Tyr Lys Lys His Ile Met Arg
705 710 715 720

Val Asn Pro Asn Gly Thr Arg Gln Thr Ala Ile Gly Lys Leu Ile Leu
725 730 735

Ser Thr Asp Pro Ser Thr Leu Arg Gln Gln Met Lys Gly Ser Pro Ile
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His Val Ile Asp Ser Tyr Gly Ser Leu Asp Thr Gln Phe His Val Leu
900 905 910

Lys Ala Asn Thr Val Ser Gln Leu Ile Lys Phe Ala Asp Asn Asp Leu
915 920 925

Asp Ser Glu Leu Lys His Tyr Leu Val Gly Gly Asp Leu His Ser Lys
930 935 940

Gln Ala Pro Gln Cys Ser Ile Lys Leu Leu Cys Lys Cys Ile Tyr Arg
945 950 955 960

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His Leu Glu Leu Ala Leu Lys Tyr Trp Met Ser Lys Gln Gln Ser Val
995 1000 1005

Ala Ala Leu Phe Ala Met Ile His Gly Leu Ala Ala Lys Val Thr Val
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Ala Gln Thr Leu Asn Glu Gln Arg Leu Ile Leu Glu Arg Gly Ala Arg
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Asn Leu Ile Ser Val Met Glu Thr Ile His Met Thr Ser His Ser Tyr
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Gln Pro Ala Leu Leu Gln Leu Gln Val Met Ala Asn Arg Arg Asp Met
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Asn Ser Thr Leu Asp Leu Ala Gly Phe Ser Ile Leu Gln Ser Glu Asp
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Ser Met Tyr Trp Met Glu Lys Ser Tyr Leu Met Glu Leu Glu Asp Ser
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Trp Asn Asp Leu Lys Trp Leu Glu Lys Leu Gln Glu Met Trp Arg Leu
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Ser Lys Tyr Ser Ile Ser Gly Ile Ser Gln Leu Ser Met Lys Gly Ala
1125 1130 1135

Thr Asp Leu Gly Gly Arg Tyr Ser Val Ser Ala Lys Gln Phe Ile Thr
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Ser Val Met Lys Pro Val Lys Lys Ser Cys Val Lys Ala Arg Asp Thr
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Cys Lys Glu Val Ile Ile Asn Thr Thr Ser Trp Thr Phe Arg Ala Thr
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Phe Ser Leu Cys Arg Trp Cys Leu Pro Asp Cys Leu Lys Phe Ile Asn
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Met Leu Ile Val Ile Ser Leu Ile Leu Ser Ile Trp His Ser Ala Asn
1205 1210 1215

Ser Ile Ser Phe Asp Tyr Ala Gln Met Lys Arg Glu Lys Gln Val Asn
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Ile Glu Lys Val Leu Met Asn Asn Leu Val Ala Leu His Lys Glu Gln
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Ile Lys Ile Asn Pro Asp Leu Thr Lys Glu Glu Phe Lys Glu Tyr Ile
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Ala Arg Ser Arg Pro Glu Leu Ile Ala Leu Val Asn Lys Glu Leu Gln
265 1270 1275 1280

Glu Glu Val Asp His Gln Ala Lys Arg Lys Gly Glu Gln Asn Leu Glu
1285 1290 1295

Lys Ile Ile Ala Phe Val Ala Leu Val Met Met Ile Phe Asp Ser Glu
1300 1305 1310

Lys Ser Asp Cys Val Tyr Lys Thr Leu Asn Lys Leu Arg Asn Leu Val
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Ala Thr Cys Asp Glu Pro Val Ala His Gln Ser Leu Asp Asp Ile Gln
1330 1335 1340

Asp Ile Leu Thr Asp Lys Glu Thr Thr Ile Asp Phe Asp Leu Asp Cys
345 1350 1355 1360

Glu Gly Ser Lys Val Thr Glu Phe Lys Glu Met Asn Phe Ala Ala Trp
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Trp Glu Lys Gln Leu Gln Cys Asp Arg Val Val Pro His Tyr Arg Thr
1380 1385 1390

Thr Gly Lys Phe Ile Glu Phe Thr Arg Glu Ser Cys Val Ser Val Ser
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Asn Thr Ile Ser His Ala Pro Glu Lys Glu Trp Ile Val Arg Gly Gly
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Val Gly Ser Gly Lys Ser Thr Gly Leu Pro Phe Ala Leu Ser Ser Lys
425 1430 1435 1440

Gly Ala Val Leu Met Leu Glu Pro Thr Arg Pro Leu Ala Glu Asn Val
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Ser Arg Gln Leu Arg Gln His Pro Phe Tyr Ala Asn Pro Thr Leu Arg
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Met Arg Gly Met Ser Ser Phe Gly Ser Ser Asn Ile Cys Ile Met Thr
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Ser Gly Phe Ala Phe Asn Tyr Phe Ala Asn Asn Pro Leu Lys Leu Ser
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Asp Phe Glu Phe Val Ile Ile Asp Glu Cys His Val Leu Asp Ser Asn
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Ala Met Ala Phe Val Cys Leu Leu Lys Glu His Asn Tyr Asp Gly Lys
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Leu Leu Lys Val Ser Ala Thr Pro Gln Gly Arg Glu Cys Glu Phe His
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Thr Gln His Pro Val Ser Ile His Ile Glu Glu Gln Leu Ser Phe Gln
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Ala Phe Cys Glu Ala Gln Gly Thr Gly Ser Ala Arg Asp Val Ile Asn
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Lys Gly Asp Asn Ile Leu Val Tyr Val Ala Ser Tyr Asn Glu Val Asp
585 1590 1595 1600

Gln Leu Ser Lys Met Leu Gly Asp Lys Gly Tyr Leu Val Thr Lys Val
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Asp Gly Arg Thr Met Lys Ile Gly Ser Thr Asp Ile Val Thr Lys Gly
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Ser Ser Gln Lys Lys His Phe Ile Val Ala Thr Asn Ile Ile Glu Asn
1635 1640 1645

Gly Val Thr Leu Asp Val Asp Val Val Val Asp Phe Gly Leu Lys Val
1650 1655 1660

Thr Ala Glu Ile Asp Tyr Asp Asn Arg Cys Val Asn Tyr Thr Lys Thr
665 1670 1675 1680

Ser Ile Ser Tyr Gly Glu Arg Ile Gln Arg Leu Gly Arg Val Gly Arg
1685 1690 1695

His Lys Lys Gly His Ala Met Arg Ile Gly Thr Thr Ile Lys Gly Leu
1700 1705 1710

Ile Glu Ile Pro Ser Leu Val Ala Thr Gln Ala Ala Phe Gln Cys Phe
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Thr Tyr Gly Leu Pro Val Met Thr Gln Gly Val Ser Val Asn Ser Leu
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Ser Asn Cys Thr Val Arg Gln Ala Arg Val Met Ser Arg Phe Glu Leu
745 1750 1755 1760

Pro Pro Tyr Phe Met Ala Ser Leu Val Tyr His Asp Gly Ser Met His
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Pro Glu Ile His Lys His Leu Ile Pro Tyr Lys Leu Asp Glu Ser Glu
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Ile Gln Leu Ser Ala Met Ala Phe Asn Phe Thr Val Thr Ser Ile Trp
1795 1800 1805

Leu Asp Cys Lys Phe Tyr Asp Ser Ile Gly Ile His Leu Asp Leu Pro
1810 1815 1820

Arg Glu Ala Lys Ile Pro Phe His Cys Arg Glu Phe Pro Asp Met Lys
825 1830 1835 1840

Tyr Arg His Leu Trp Glu Asp Ile Leu Lys Ile Lys Ser Ile Asn Cys
1845 1850 1855

Phe Gly Arg Met Ser Val Val Ser Ala Thr Lys Val Ala Tyr Thr Leu
1860 1865 1870

Lys Thr Asp Ile His Ser Ile Gly Lys Thr Leu Gly Tyr Ile Asp Ala
1875 1880 1885

Leu Leu Gln Glu Glu Tyr Arg Lys Gln His His Phe Lys Ala Met Thr
1890 1895 1900

Ser Asn Ala Cys Ser Gly Asn Thr Phe Ser Met Leu Ser Ile Ala Asn
905 1910 1915 1920

Ala Ile Arg Asn His Tyr Ala Lys Asp Tyr Thr Ala Gly Asn Ile Gln
1925 1930 1935

Lys Leu Gln Ala Ala Lys Asn Gln Ile Leu Glu Phe Val Asn Leu Asn
1940 1945 1950

Leu Asp Pro Ser Ala Lys Cys Gly Phe Gln Glu Phe Gly Ala Leu Glu
1955 1960 1965

Leu Val Thr His Gln Ser Arg Gln Glu Ile Ser Lys Phe Leu Asn Leu
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Arg Gly Lys Trp Asn Lys Ser Leu Ile Thr Arg Asp Ile Leu Val Leu
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2005 2010 2015

Ser Asn Ile Glu Glu Val His His Glu Gly Lys Arg Lys Thr Gln Lys
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Val Asp Leu Gln Pro His Asn Pro Leu Leu Ile Cys Lys Asn Lys Ala
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Lys Ala Tyr Glu Val Ser Arg Glu Glu Leu Pro Glu Arg Asn Glu Asp
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Val Ser Phe Glu Gly Ala Ser Ser Val Lys Gly Leu Arg Asp Tyr Asn
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Gly Val Ala Ser Ala Ile Cys Gln Leu Thr Asn Asn Ser Asn Gly Arg
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Lys His Trp Ile Asn Thr Thr Glu Gly His Cys Gly Leu Pro Leu Val
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Asn Gln Leu Glu Gly Asn Leu Lys Ala Val Ala Thr Ile Pro Asn Asn
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Phe Val Thr Lys His Ile Val Lys Gly Arg Cys Lys Leu Phe Glu Leu
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Val Lys Pro Glu His Arg Leu Glu Ala Ile Cys Ala Ser Met Ile Glu
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Tyr Gly Val Gly Phe Gly Ser Tyr Ile Ile Val Asn Arg His Leu Phe
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Lys Glu Asn Asn Gly Asn Leu Leu Ile Lys Ser Thr His Gly Asn Phe
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aat atc agg aac tcc aag caa att aaa gtc gtc gga gtg gag gat agg 240
Asn Ile Arg Asn Ser Lys Gln Ile Lys Val Val Gly Val Glu Asp Arg
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gat att gcc att ctt caa atg cct aaa gac ttc cca ccc ttt gca cag 288
Asp Ile Ala Ile Leu Gln Met Pro Lys Asp Phe Pro Pro Phe Ala Gln
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Arg Leu Arg Phe Arg Asn Pro Ile Val Gly Glu Ser Ile Cys Leu Val
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Gly Asn Thr Phe Gln Glu Lys Tyr Asn Ala Ser Ile Val Ser Glu Thr
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Ser Lys Thr Phe Pro Arg Val Glu Gly Ser Phe Trp Lys His Trp Ile
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Asn Thr Thr Glu Gly His Cys Gly Leu Pro Leu Val Ser Val Thr Asp
145 150 155 160

gga ttt att gta gga ata cat agt tta atg agt cat aag tac gat cat 528
Gly Phe Ile Val Gly Ile His Ser Leu Met Ser His Lys Tyr Asp His

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Asn Tyr Phe Ser Asn Phe Asp Asp Ala Phe Glu Gly Asp Tyr Ile Asn
180 185 190

aag ttg aag gaa ctg aaa tgg gag cag aat tgg act tac aac gtt aat 624
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Cys Ala Gln

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35 40 45

Lys Glu Asn Asn Gly Asn Leu Leu Ile Lys Ser Thr His Gly Asn Phe
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Asn Ile Arg Asn Ser Lys Gln Ile Lys Val Val Gly Val Glu Asp Arg
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Arg Leu Arg Phe Arg Asn Pro Ile Val Gly Glu Ser Ile Cys Leu Val
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Gly Asn Thr Phe Gln Glu Lys Tyr Asn Ala Ser Ile Val Ser Glu Thr
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Ser Lys Thr Phe Pro Arg Val Glu Gly Ser Phe Trp Lys His Trp Ile
130 135 140

Asn Thr Thr Glu Gly His Cys Gly Leu Pro Leu Val Ser Val Thr Asp
145 150 155 160

Gly Phe Ile Val Gly Ile His Ser Leu Met Ser His Lys Tyr Asp His
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Asn Tyr Phe Ser Asn Phe Asp Asp Ala Phe Glu Gly Asp Tyr Ile Asn
180 185 190

Lys Leu Lys Glu Leu Lys Trp Glu Gln Asn Trp Thr Tyr Asn Val Asn
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Thr Val Ser Trp Gly Asn Met Lys Leu Gln Asp Ser Ala Pro Cys Lys
210 215 220

Glu Phe Lys Thr Thr Lys Leu Ile Ser Asp Leu Cys Thr Glu Pro Val
225 230 235 240

Cys Ala Gln

[Name of Document] ABSTRACT

[Abstract]

[Problems] The purpose of the present invention is to determine the nucleotide sequence of the full-length genomic RNA of papaya leaf-distortion mosaic virus.

[Means for Solution] The full-length genomic RNA of papaya leaf-distortion mosaic virus, a method for diagnosing infection with papaya leaf-distortion mosaic virus using the full-length genomic RNA, a method for producing a papaya leaf-distortion mosaic virus-resistant plant, and a method for producing a foreign protein in a plant body.

[Selected Figure] None